

Inflammatory Modulation in Sepsis – Role of Adenylyl Cyclases



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Abbreviations

A

A2A	Adenosine 2A
A2B	Adenosine 2B
AC	Adenylyl cyclase
AKAP	A-kinase anchoring proteins
ATF	Activating transcription factor

B

BPM	Beats per minute
BCL-3	B-cell lymphoma 3

C

cAMP	Cyclic adenosine 3',5'-monophosphate
CARS	Compensatory anti-inflammatory response syndrome
CBP	CREB-binding protein
CREB	cAMP responsive element binding TF
CHF	Chronic heart failure
CLP	Cecal ligation and puncture
COPD	Chronic obstructive pulmonary disease
COX	Cyclooxygenase
CR	Complement receptor

D

DAMP	Danger-associated molecular pattern
DNA	Deoxyribonucleic acid

E

EBV	Epstein-Barr virus
EPAC	Exchange protein directly activated by cAMP

F

FADD	Fas-associated protein with death domain
FcR	Fragment, crystallizable region

G

GC	Granulocyte
GEF	Guanine nucleotide exchange factor
GM-CSF	Granulocyte-macrophage colony-stimulating factor
GPCR	G-protein coupled receptor
GTP	Guanine triphosphate

H

HIV	Human immunodeficiency virus
HMGB-1	High mobility group box-1

I

ICAM	Intracellular adhesion molecule
ICU	Intensive care unit
IFN	Interferon
IκB	Inhibitory kappa-light-chain-enhancer of activated B cells
IKK	IκB kinase
iNOS	Inducible nitric oxide synthase
IL	Interleukin
IRAK	IL-1 receptor-associated kinase
IRF	Interferon regulatory factor

J

JAK/STAT	Janus kinase/signal transducer and activator of transcription
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K

KC	Kupffer cell
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L

LBP	LPS-binding protein
LPS	Lipopolysaccharide
LRR	Leucine-rich repeat
LSEC	Liver sinusoidal endothelial cell
LTA	Lipoteichoic acid
LV	Left ventricle

M

MAMP	Microbial-associated molecular pattern
MARS	Mixed anti-inflammatory response syndrome
MCP	Monocyte chemoattractant protein
MHC	Major histocompatibility complex
MIP	Macrophage inflammatory protein
MMIF	Macrophage migration inhibitory factor
MPO	Myeloperoxidase
MTOC	Micro-tubuli organizing center

N

NF-κB	Nuclear factor kappa-light-chain-enhancer of activated B-cells
NK	Natural killer
NOD-LRR	Nucleotide-oligomerization domain leucine-rich repeat

P

PACAP	Pituitary adenylyl cyclase activating polypeptide
PAF	Platelet activating factor
PDE	Phosphodiesterase
PepG	Peptidoglycan
PKA	Protein-kinase A
PG	Prostaglandin
PAMP	Pathogen-associated molecular pattern
PBMC	Peripheral blood mononuclear cell
PLB	Phospholamban
PRR	Pattern recognition receptor

R

RISC	RNA-induced silencing complex
RNA	Ribonucleic acid
RNP	Ribonucleo protein
RLH	Retinoic-acid-inducible gene I (RIG-I)-like helicases
ROS	Reactive oxygen species
RT-PCR	Reverse-transcriptase polymerase chain reaction

S

SERCA	Sarco/endoplasmic reticulum Ca^{2+} -ATPase
SIRS	Systemic inflammatory response syndrome
SOCS	Suppressor of cytokine signaling

T

TIR	Toll/interleukin-1 receptor
TLR	Toll-like receptor
TNF	Tumor necrosis factor
TRAF	TNF-receptor-associated factors
TGF	Transforming growth factor
TRAM	Trif-related adaptor molecule
TRIF	TIR-domain-containing adapter-inducing interferon-β

U

UTR	Untranslated region
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W

WBC	White blood cells
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1. List of papers

Paper I

Risøe PK, Wang YY, Stuestøl JF, Aasen AO, Wang JE, Dahle MK. *Lipopolysaccharide attenuates mRNA levels of several adenylyl cyclase isoforms in vivo*. Biochem. Biophys. Acta 2007 Jan;1772(1):32-9.

Paper II

Risøe PK, Ryg U, Wang YY, Rutkovskiy A, Smedsrød B, Valen G, Dahle MK. *Cecal ligation and puncture sepsis is associated with attenuated expression of adenylyl cyclase 9 and increased miR142-3p*. Shock 2011 Oct;36(4):390-5.

Paper III

Risøe PK, Rutkovskiy A, Ågren J, Kolseth IB, Flood Kjeldsen S, Valen G, Vaage J, Dahle MK. *Gender differences in TNF α responses are associated with attenuated adenylyl cyclase expression in male monocytes*. Manuscript submitted for publication.

2. Introduction

2.1 Sepsis and the cytokine theory of disease

Sepsis is a serious medical condition characterized by systemic inflammatory responses triggered by infection, at its most dramatic a process transforming from traceable bacteremia to cataclysmic loss of vital organ function and death within 24 hours. The mortality of severe sepsis with organ dysfunction ranges from 30 to 50%, and according to data from the Centers for Disease Control, it features as the leading cause of non-coronary fatalities in the intensive care unit (ICU) (1). Norwegian estimates operate with an annual incidence of 6000 patients, accounting for approximately 100.000 days of hospital admissions (2).

Sepsis was poorly understood until the early 1970s, when it became clear that manifestations of sepsis could not be solely accounted for through the direct actions of pathogenic toxins. Challenging previously held beliefs assuming the inflammatory response to be uniformly for good, investigations exploring the mechanisms of fever and the acute phase pointed towards proteins produced by macrophages and other immune cells, not pathogens themselves, as a major causative factor underlying tissue damage and organ dysfunction (3). It soon became evident that any understanding of the sepsis phenomena would have to incorporate the host endogenous response as a crucial component of the pathophysiology. These insights led to the eloquent and prescient formulation put forth by a contemporary pioneer, Lewis Thomas:

“When we sense lipopolysaccharide, we are likely to turn on every defense at our disposal; we will bomb, defoliate, blockade, seal off, and destroy all the tissues in the area... The self-disintegration of the whole animal can be interpreted as a well-intentioned but lethal error. The mechanism is itself quite a good one, *when used with precision and restraint*” (4)

Today, the notion of an exaggerated pro-inflammatory mediator production as a driving force in the pathophysiology of not only sepsis, but other forms of shock as well, has been commonly accepted as the *cytokine theory of disease*. Leaping out of reasonable proportions, the overwhelming production of inflammatory mediators set off a cascade of leukocyte infiltration, endothelial dysfunction, circulatory collapse, hemorrhagic necrosis, multiple organ failure and other physiological calamities (5). However, while our understanding of sepsis has been radically altered over the last three decades, this shift in paradigms has made only modest contributions to its treatment. Current

standard of care remains early goal-directed resuscitation, blood cultures, identifying the source of infection, institution of broad antibiotic regimens and supportive care in the ICU (6). Although considerable gains are possible by way of a more rigid implementation of these principles worldwide, there is an ostensible and dire need for other and more effective approaches in the fight against sepsis (7).

2.2 Innate immunity and sepsis

2.2.1 A brief introduction to innate immunity

The importance of innate immunity for viability in a world dominated by microorganisms is underscored by the early evolutionary origins of the system, which can be traced back to early eukaryotes such as the amoeba. By the time organisms diverged into plants and animals, the main elements of specific pathogen-mediated generic immune responses (e.g. the Toll pathway and NF- κ B) had already been hardwired into the genome. This consistency of function, structure, order and purpose over such a wide evolutionary range is one of the most impressive examples of conserved ancient evolution (8).

The ingenuity of evolution answered the threat of microbial enemies by developing a defense system based on recognizing unique structural constituents of fundamental importance for the invading microorganisms. Now referred to as pathogen-associated molecular patterns (PAMPs), or sometimes more appropriately microbial-associated molecular patterns (MAMPs) as they are also present in common non-pathogenic organisms, they initiate the innate immune response by binding to pattern-recognition receptors (PRRs) on host cell surfaces (9). Later, the system provided a foundation for the development of additional capacity to detect generic endogenous danger signals (known as danger-associated molecular patterns, or DAMPs) indicating tissue injury, such as heat shock proteins, fibrinogen, fibronectin, hyaluronan, biglycans and high-mobility group box-1 (HMGB1) (10). During pathogen invasion or non-infectious injury such as trauma, PAMPs and DAMPs trigger the activation of different PRRs: 1) Toll-like receptors (TLRs); 2) NOD-LRR; 3) C-type lectins; and 4) cytoplasmic caspase activation and recruiting domain helicases such as RLFs (9). While NOD was originally suggested to act as direct sensors, they are now also thought to function as switches and cellular assembly blocks for such signals of cellular distress, leading to the generation of various multiprotein inflammasomes crucial for inflammatory mediator processing (11;12).

Recognition of cognate activation signals by sentinel immune cells such as tissue macrophages, which are strategically stationed at microbial entry points, result in the production of pro-inflammatory

mediators aimed at attracting more immune cells to the site (8). The recruitment of more activated phagocytes to sites of infection is one of the most important functions of innate immunity. Endothelial permeability and cell-adhesion molecules in vessel walls swiftly increase in order to facilitate this migration towards the foreign invader (discussed more extensively later).

Monocytes are a subset of circulating immune cells that traffic via the blood stream to peripheral tissues, either replenishing stationary tissue macrophages, or when called upon, engage in eradication of pathogens (13). First-responder macrophages that recognize PAMPs or DAMPs call for help by secreting pro-inflammatory cytokines like TNF α , IL-1, IL-12 and IL-23, release chemokines to guide the recruited cells, secrete nitric oxide as part of antimicrobial oxidative processes, and engage in phagocytosis. Depending on the local milieu, macrophages can differentiate into antimicrobial M1 macrophages or wound-healing M2 macrophages; the latter also produce anti-inflammatory cytokines that help resolve and limit inflammation (14).

Granulocytes are the first and most numerous cells to be recruited to infected tissue, and carry storage granules containing proteases that degrade connective tissue in order to allow cells to enter the site of infection, and antimicrobial compounds to effectively neutralize a foreign threat. Neutrophils, the most numerous of the circulating leukocytes, swarm to the site of infection after sensing chemokines, and goes on to release an arsenal of constituents crucial to host defense; a virtual bombardment of reactive oxygen species, antimicrobial peptides, and serine proteases that may destroy not only bacterial and fungal pathogens, but the surrounding tissue as well (15). Mast cells in connective tissue and mucous membranes degranulate within seconds of activation, releasing an array of proteases (thought to be an important part of parasitic defence) and histamine, which initiates vasodilatation and increased vascular permeability to facilitate extravasation of arriving phagocytic cells (16). In addition, mast cells produce eicosanoids, several proinflammatory cytokines and a number of chemokines augmenting the further recruitment of immune cells. Basophils may act synergistically with mast cells in releasing histamine, and eosinophils, recruited by eotaxin chemokines, release free radicals and cytotoxic cationic proteins aimed at fighting pathogens (17;18).

For intracellular pathogens, other strategies are needed. Natural killer (NK) cells terminate other cells that fail to display proper MHC markers at their surface ("missing self"), as this could indicate that they are either broken (e.g. tumor cells) or infected by virus (19). The cytotoxic cells (NK cells, NKT-cells) primarily act by inducing apoptosis or cell lysis in cells that lack proper molecular identification, but also produce an antimicrobial capable of destroying bacteria, eukaryotic cellular pathogens and

parasitic cells by disruption their cell wall (20-23). Dendritic cells and $\gamma\delta$ T-cells both serve as bridges to the adaptive immune system (24;25).

The innate immune cells also interact with other defensive mechanisms. For example, the complement system can be cross-activated through inflammatory activation by multiple pathways: either through C3b-binding to the microbe (the alternate pathway), by binding mannose sugars or opsonins on bacterial surfaces (the mannose-binding lectin pathway) or through TLR-C5a crosstalk (26;27). Complement C5a amplifies the production and release of proinflammatory cytokines, enhances phagocytosis in phagocytic cells, stimulates oxidative bursts and granular release in granulocytes, activates the coagulation cascade by inducing tissue factor and acts as a potent vasodilator while increasing the expression of endothelial adhesion molecules (27).

2.2.2 The TLR signaling pathway

Ten mammalian TLRs have been identified since the discovery of the original Toll receptor in the *Drosophila* fruitfly, and in both families, these PRRs have proved to be of critical importance to the innate immune response (28;29). TLRs are glycoproteins consisting of an extracellular domain containing 16-28 leucine-rich repeat (LRR) modules, a transmembrane domain and an intracellular TIR signaling domain. A large variety of PAMPs induce hetero- or homologous dimerization of the receptors, triggering structural change leading to the recruitment of adaptor proteins to the intracellular Toll/interleukin-1 receptor (TIR) domains (30-32).

TLR4 is the sensor for lipopolysaccharide (LPS), and due to the focus of this thesis, it will serve as an illustration of a TLR signaling process. In conjunction with its coreceptor MD2, TLR4 is specific for lipid A, the main inducer of biological responses to LPS (33-35). The LPS molecule bind exclusively to MD2, and TLR4 and MD2 interaction is mediated mainly by ionic and hydrogen bonds in two oppositely charged patches (36;37). Ligand binding induces the dimerization of the complex, and subsequently initiates signaling. In addition, two accessory proteins are needed to recognize LPS at physiological concentrations (38-40). Plasma LPS-binding protein (LBP) extracts LPS from the outer membrane of Gram-negative bacteria or from vesicles continually shed during bacterial growth, and transfers it to CD14 in a monomeric form (41). Upon binding, two CD14s, which can exist in a soluble form or as a GPI-anchored protein on the cell membrane, form a dimer containing 22 LRR modules which in shape and size appear to be comparable to the TLRs (42;43). Because CD14 has no intracellular signaling domain, LPS is transferred to the TLR4-MD2 complex to initiate immune responses (36;41). Dimerization of the extracellular domains of the activated TLR4-MD2 complex is then thought to

induce dimerization of the intracellular TIR domains, leading to proper orientation or conformational change allowing for downstream signaling mediation (36).

The signaling cascade initiated by activation of the TIR dimers elicits major transformations of cellular transcription. Broadly, two key regulators of inflammation – Nuclear factor kappa-light-chain-enhancer of activated B-cells (NF- κ B) and Interferon regulatory factor (IRF) 3 – are activated by the recruitment of two sets of adaptor proteins initiating different signaling pathways; MyD88/Mal and TRIF/TRAM, respectively (44-46). IRF3 activation typically induces interferons (IFNs) implicated in anti-viral defense, and will not be further discussed in this thesis. MyD88 protein and IL-1R associated kinase pathways activate NF- κ B, a transcription factor constituted by homo- and heterodimers of the Rel protein family. Latent NF- κ B molecules are sequestered in the cytoplasm by I κ B proteins. TLR-activation induces degradation of the I κ Bs in proteasomes, unmasking the nuclear localization signal of NF- κ B and resulting in nuclear translocation, binding to NF- κ B motifs and the transcription of more than 150 genes. NF- κ B is considered a key switch for changing the intracellular physiology from its normal steady-state to inflammatory activation (9).

The engagement of TLR4 by LPS and the subsequent signal transduction has been demonstrated to turn on more than a thousand genes, of which more than 75 % are MyD88-independent (47). Within the scope of a few hours, the gene expression profile of the activated innate immune cell is radically transformed following the recognition of a PAMP or DAMP signal. The first category (class I) of transcription factors induced by PRR binding occurs within 0.5-2 hours, and controls the induction of the primary response genes, including NF- κ B, IFN-regulatory factors and cAMP-responsive-element-binding protein 1 (48). These initial transcription factors are activated by posttranslational modification and nuclear translocation after the PRR signal. The second round of transcription occurs from 2 to 8 hours past the initial receptor binding, and depends on (class II) transcription factors induced during the primary response, as well as secondary response genes. Among the proteins resulting from this second round of activation are some of the most well-known pro-inflammatory mediators; tumor necrosis factor α (TNF α), interleukin (IL)-1, IL-6, and IL-12, monocyte chemoattractant protein (MCP), macrophage inflammatory protein (MIP)-1 α and -1 β , and inducible nitric oxide synthase (iNOS) and cyclooxygenase (COX)-2 (49-53). In the secondary response, which take place post 8 hours after first contact, the LPS-inducible negative feedback loops are activated and the molecular picture changes towards a state of anti-inflammation, with release of anti-inflammatory cytokines such as transforming growth factor (TGF) β and IL-10, nuclear hormone receptors such as liver X receptors (LXRs), peroxisome proliferator-activated receptors (PPARs), vitamin D receptors, and cAMP (48). The nuclear receptors integrate the control of inflammation

with various physiological functions, such as metabolism, and inhibit inflammation through multiple mechanisms. Inducible negative regulators working at the transcription level of primary response genes are also upregulated; most importantly, I κ BNS (controls IL-6, IL-12, and IL-18) and B cell lymphoma 3 (BCL-3, which controls TNF, IL-10 and IL-1 β) (48).

TLR expression is significantly up-regulated in patients with sepsis, as well as in states abundant in DAMPs (e.g. trauma, thermal injury) (54-57). It has been proposed that TLR augmentation primes the innate immune system for enhanced TLR reactivity, predisposing to an observed increase in LPS-mediated mortality after DAMP-intensive events (58). The existence of positive feedback loops between DAMPs and PAMPs may represent the molecular basis for the phenomenon that infections, traumas and nonspecific stress factors sometimes triggers flares of systemic inflammation, accompanied by baleful consequences if they spiral out of control (9;55;59).

2.2.3 SIRS, MARS and CARS

When fighting off foreign invaders or reacting to signals of endogenous tissue damage, the innate immune system operates as a cascading process that includes the activation of cells with the potential to cause considerable collateral damage to surrounding tissues as they indiscriminately barrage their environment with reactive oxygen species, antimicrobial peptides, and serine proteases. If the site of infection is extensive enough, dead bacteria and host cells both release vast amounts of PAMPs and DAMPs in the blood stream, which together with the increasing levels of pro-inflammatory cytokines produced locally serve to activate systemic inflammatory responses, such as fever, acute phase protein release, and reinforcement of the pro-inflammatory signal through the outpouring of cytokines from sources beyond the local tissue, such as endothelial cells, circulating monocytes or even remote tissue macrophage populations such as the Kupffer cells of the liver (60).

Clinically, the spill-over from local to systemic, which in severe cases can be viewed as loss of control over the pro-inflammatory cascade, can result in a condition referred to as the systemic inflammatory response syndrome (SIRS): heart rate > 90 bpm; body temperature < 36 or > 38 °C; tachypnea > 20 breaths per minute or P_aCO₂ < 4,3 kPa; WBC count < 4 x 10³ or > 12 x 10³ cells/mm³ or > 10 % immature neutrophils). This clinical definition is generally taken to reflect systemic inflammation where no definite source of infection has been identified (61). Although it is generally agreed that its positive predictive value is unsatisfactory and more elaborate diagnostic consensus criteria for sepsis have been developed, for the purposes of this thesis is it sufficient to use the putative rule of thumb that sepsis is SIRS with an infectious cause (62).

In the course of our present decade, the *cytokine theory of disease* and its concept of SIRS have been supplemented, albeit not directly challenged, by the concepts of mixed anti-inflammatory response syndrome (MARS) and compensatory inflammatory response syndrome (CARS). Incorporating the fact that most patients receiving current standard of care do not die from the initial septic insult, but more often from a “second” or “third hit” caused by secondary infection acquired during their stay in the ICU, this model presumes that the overproduction of pro-inflammatory mediators evolves into a state with high signaling activity on the part of both pro- and anti-inflammatory cytokines, MARS. Subsequently, MARS gradually gives way to a more prolonged homeostasis characterized by exaggerated anti-inflammatory release causing severe immunodepression, CARS, predisposing for secondary infections and renewed bouts of disease activity in the already torpid patient (63;64).

This reappraisal of Lewis Thomas theory of uncontrolled hyperinflammation as the sole contributor to septic shock pathophysiology is based on a substantial evidence showing that most septic patients went to a situation of dysregulated and debilitated innate immune responses. Often referred to as immunoparalysis, the condition was found to last from three to seven days in monocytes after trauma [163]. During this period, activated CD4 helper T cells undergo a shift in their secretion of cytokines, and the initial release of pro-inflammatory cytokines such as TNF α , IFN γ and IL-2 produced while the cell is in type 1 (Th1) mode gives way to the antagonistic type 2 (Th2) mode, where production of anti-inflammatory IL-4 and -10 dominates (64). Both in human and animal models, CARS has been characterized by a cytokine profile of predominantly anti-inflammatory nature, monocyte deactivation, dysfunction of dendritic cells, impairment of neutrophils, and lymphocytic anergy and apoptosis (65;66).

However, the orderly model of MARS and CARS is poorly supported by clinical or *in vivo* evidence (67). An experimental animal study examined the inflammatory alterations preceding lethality in late sepsis, failing to find evidence supporting a linear connection between SIRS, MARS and CARS (68). This publication strengthened the claim that mechanisms leading to death in the early, pro-inflammatory shock differ from death during the later, hypoinflammatory stage (69). Instead, the SIRS-to-CARS transition may rather be a constantly fluctuating oscillation between hyper- and hyporesponsiveness in different patients (65).

2.2.4 Gender aspects of sepsis

Numerous articles point to a gender dimorphism in the susceptibility for and morbidity from sepsis, although the precise role of gender has been subject to considerable controversy and conflicting reports (70-81). Sepsis, itself a catch-all term for what may represent more than one immunological

disequilibrium, are associated not only with a wide range of confounding factors, such as lifestyle activities, risk behaviors, ethnicity, local microbial flora, but also healthcare access and delivery. Although most English-language articles in the field report gender as a demographic variable, only a minority examine the effects of gender on health outcomes (82). Some authors have suggested that gender differences in symptoms, presentations of illness, or diagnostic bias make women are less likely to receive advanced intensive care interventions, and a number of the studies do demonstrate the existence of a gender disparity in treatment (72;76;78).

The data on effects of sex hormones on the various components of human immunity *in vivo* is conflicting, suggesting a spectrum of cytokine production in females from both more and less pro-inflammatory action compared to males (81;83-86). However, most studies have not controlled or standardized subjects with respect to menstrual phase and hormonal contraceptives, which have both been shown to have profound effects on female immune physiology (87;88).

Among the conflicting reports on gender dimorphism on septic mortality there are two broader observations that are notable. The first is that the incidence of sepsis is considerably higher in males in a majority of the unmatched studies, suggesting that men are more likely to progress from bacteremia to sepsis relative to women (70-72;74;76;79-81;89). The second observation is that those studies examining premenopausal women separately show that they have consistently higher survival rates compared to men of comparable age (70;72;74;76;79;81). However, the survival advantage conferred by female gender appears diminished or disappeared altogether in the sixth decade of life, and some studies even indicate worse outcomes for older women (71;78;80;89). As these changes appear to correspond in time with the menopause it seems plausible that they may be related to the immunological effect of female sex hormones.

2.3 The cyclic AMP second messenger system

2.3.1 A brief introduction to the cAMP signaling system

In the 1950's Southerland and Rall detected that intracellular levels of cyclic adenosine monophosphate (cAMP) were elevated when adding hormones, and serendipitously made the first discovery of intracellular signaling. They demonstrated that cAMP is synthesized from adenosine triphosphate (ATP) by membrane-bound adenylyl cyclases (ACs), activated by transmembrane receptors via G-proteins. Sutherland was awarded the 1971 Nobel Prize for his work, which would prove to be the first of five Nobel Prizes recognizing research on this molecule (90). Half a century

later, the cAMP signaling pathway is referenced as the archetypical second messenger system, regulating a wide range of functions in all mammalian cells in a precise and specific manner.

With one exception, the AC isoforms are all membrane-bound and regulated by extracellular signals through transmembrane G-protein coupled receptors (GPCRs) and G-proteins. Hundreds of different GPCRs exist, but it has revealed that the interactions between certain GPCRs and ACs at the cellular level is highly specific (91). Simplifying greatly, G-proteins (each made up of an α , β and γ subunit) released by an activated receptor are classified according to whether they stimulate (Gs) or inhibit (Gi) cAMP production (92). Some ligands best known for their activation of Gs-coupled GPCR ligands include epinephrine, norepinephrine, nicotine, histamine, serotonin and certain COX-derived prostaglandins (particularly PGE₂ and I₂, the latter also known as prostacyclin), while examples of Gi-coupled GPCR ligands are chemokines CCR1-1 and CXCR1-6, as well as leukotrienes B₄, C₄ and D₄ (93). Recently, it has been revealed that GPCRs may continue their signaling via the cAMP system after being internalized (94).

The ten isoforms of AC are countered by more than 40 different phosphodiesterase (PDE) isozymes (95), which through distinct expression and regulatory profiles together tune the levels of cAMP in the cell. PDEs and cAMP target proteins can associate with the AC-G-protein membrane complexes, forming defined subcellular compartments where a localized pool of cAMP exerts its effects (91;95). The diversity of cAMP effector molecules, as well as lipid rafts, scaffolding, adaptor and anchoring proteins, contributes to the complexity of the pathway (96-98). A number of methods have now been developed to study such microdomains at the single-cell level (97;99). Simplified illustrations demonstrating different cAMP signaling routes are shown in Figure 1.

There is ample scientific evidence for highly divergent, if not completely opposite, functions of the different downstream elements to cAMP; the protein kinase PKA, the guanine nuclear exchange factor Exchange protein activated by cAMP (EPAC) and cyclic nucleotide-gated ion channels. Ion channels dependent on cAMP has been found in diverse tissues for Na⁺, K⁺, Ca²⁺, Cl⁻ and HCO₃ channel function (100-102). Cyclic nucleotide gated ion channels are regulated directly by the binding of cAMP to their cytoplasmic tail, and A-kinase anchoring proteins (AKAPs) seem to be essential in creating the necessary microenvironments for this to happen (103-105). Also, specific cAMP analogues have been developed to activate PKA and EPAC separately, which has given rise to studies allowing for their separate study (102;106).

Together, these discussed features give the cAMP signaling system flexibility and spatiotemporal precision to act upon multiple intracellular processes. In different cell populations, cAMP has been

demonstrated to serve crucial signaling functions in processes as diverse as cell growth control, survival, motility, gene expression, cell-cell communication, adaptive immunity, cardiac and smooth muscle contraction, metabolism, secretory processes and memory (90;107;108). Given these pleiotropic actions of cAMP it is not surprising that pharmacological manipulation of the cAMP pathway has proven benefit in a wide range of human disease, exemplified in conditions ranging from asthma and depression to HIV infection and erectile dysfunction (109-111).

cAMP SIGNALING COMPARTMENTS

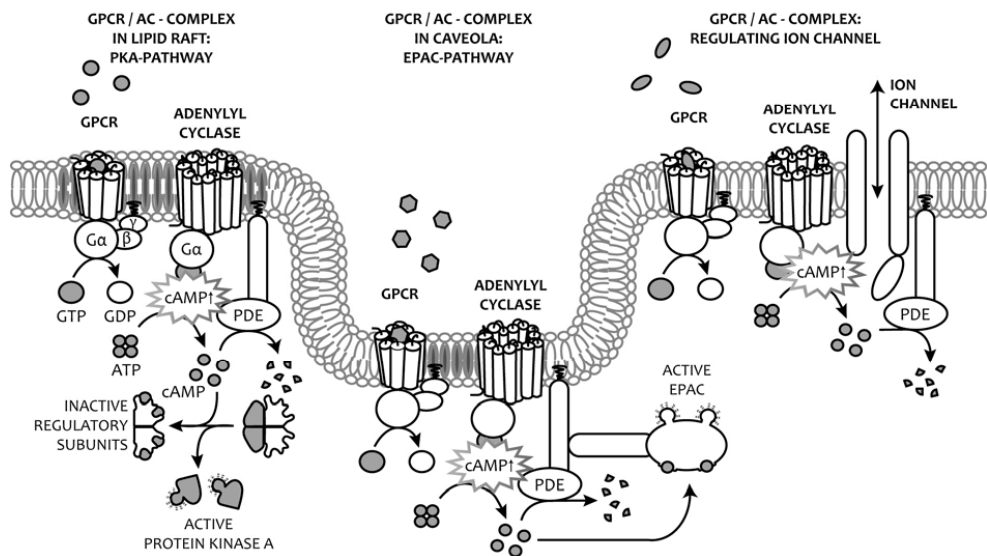


Figure 1: cAMP signaling compartments. GPCRs, ACs, PDEs and cAMP target proteins, such as PKA, EPAC or cAMP-regulated ion channels, associate and form defined subcellular signaling compartments. Please note that the configuration shown in the diagram serves just to exemplify signaling compartments and their potential localizations in the membrane, and that it is not intended to indicate a link between membrane localizations of the compartments and down-stream mediators.

2.3.2 Downstream effectors of cAMP

PKA, the first mediator to be identified, is an ubiquitously expressed heterotetramer consisting of two catalytic and two regulatory subunits (112). Two isoforms, type I and II, differ in their regulatory subunits, RI and RII respectively. In addition, four catalytic subunits have been identified by molecular cloning. All are differentially expressed, forming homo- and heterodimers, and they are likely to contribute to increased signaling specificity (113). On binding to two cAMP molecules by each regulatory subunit, the inactive tetramer dissociates into one dimer of R subunits and two active catalytic subunits that phosphorylate various target proteins (114). A-kinase anchoring proteins (AKAPs) have been shown to harbor PKA isoforms in particular subcellular compartments, associating with PDE, and upon GPCR-activation, stabilizing defined microdomains in lipid rafts or caveolae at cellular membranes (115-117). Among the main functions of PKA is the phosphorylation of the transcriptional activation domain of the cAMP-responsive-element binding protein (CREB) family of transcription factors, which then acts with cofactors such as CREB-binding protein (CBP) or p300 to initiate transcription of the CREB regulon, a collection of target genes involved in cellular processes such as proliferation, survival, differentiation and inflammatory responses (118).

In 1998, a vital step towards a fuller understanding of the cAMP signaling system was taken when EPAC was discovered as a PKA-independent signal mediator (119). Two EPACs are now known, and both are specific guanine nucleotide exchange factors (GEFs) for the Ras GTPase homologues, Rap1 and Rap2 (119;120). Like most other small GTPases, they act as molecular switches, cycling between a GDP-bound inactive and a GTP-bound active state regulated by the balance between activating GEFs and inactivating GTPase-activating proteins (GAPs). EPAC2 is predominantly expressed in the brain and adrenal gland, while EPAC1 is present in kidney, ovary, thyroid and leukocytes (92). By using the EPAC-selective cAMP analogue 8-pCTP-2-O-Me-cAMP it has been shown how a great many effects ascribed to PKA in previous publications are actually mediated by the EPAC pathways; E- and VE-cadherin-mediated cell-to-cell adhesion, integrin-mediated adhesion, monocyte chemotaxis, Ca^{2+} -induced exocytosis and FcR-mediated phagocytosis (106;114;121-126). However, despite the increasing body of evidence implicating EPAC in many of the important anti-inflammatory effects of cAMP, the exact molecular basis for these processes has yet to be elucidated.

2.3.3 Flexibility and spatiotemporal precision in the cAMP system

The fact that cAMP signals could elicit differential downstream responses was first observed more than three decades ago, and it has since become clear that the system can achieve a remarkable specificity and flexibility through spatial control of the components involved in signal transduction

(96). Up until the current decade, studies into the intracellular workings of cAMP signaling was hampered by a lack of adequate tools; however, in recent years there has been a burgeoning of techniques and biosensors allowing for investigation of localized cAMP gradients within cells (99). These have revealed an intrinsic system where macromolecular complexes such as mAKAP can serve as nodes capable of integrating multiple cAMP signals with those of calcium and MAP kinases through the creation of subcellular cAMP pools with sequestered PKA and EPAC subpopulations which act as regulators of spatially localized signaling (103;127). Different R subunits construe PKA holoenzymes with distinct physiological and biological properties, which can then sense spatially discrete pools and selectively phosphorylate downstream effectors (96). Many of the processes regulated by EPAC are modulated by PKA, and there are indications of considerable cross-talk between the two main effector pathways (128;129). PDEs provide the sole means of cAMP degradation in cells, and with more than 40 identified isoforms, they are believed to provide underpinning for the compartmentalization (127). While performing the same basic function of hydrolyzing cAMP, the individual isoforms are characterized by targeting signals which allow precise localization and an intense variety in regulatory properties (130).

Investigations of spatiotemporal aspects of the second messenger system within molecular cardiology have demonstrated how these principles can coalesce into the working fundament of a precise intracellular signaling system consisting of building blocks ubiquitously available across mammalian cell types (96;131). However, the effects of cAMP signal compartmentalization in innate immunity is for the most part still unexplored.

2.4 The role of cAMP in inflammation

Manipulation of intracellular cAMP levels has been shown to suppress innate immune functions of monocytes, macrophages and neutrophils through the modulation of three key effector functions; generation of inflammatory mediators, phagocytosis and intracellular killing of ingested pathogens (90). In addition, there is strong evidence implicating cAMP in the regulation of transendothelial migration (114).

2.4.1 Modulation of mediator generation

There is a potent inhibitory effect of cAMP signaling on the endotoxin-mediated production of the pro-inflammatory mediators TNF α and leukotriene B₄, the leukocyte attracting and activating chemokines IL-8, MIP-1 α and -1 β , and the activator of cytotoxic responses in T and NK cells IL-12 (p40), in monocytes and macrophages (132-137). This inhibition is considered to be primarily

responsible for the anti-inflammatory effect of cAMP-elevating drugs in vivo. TNF α acts as a crucial early initiator of immune responses to pathogens, and is inhibited at a transcriptional level by a mechanism which is not completely understood, but has been proposed to involve the cyclic AMP response element (CRE)-binding inducible cAMP early repressor (138). Competitive inhibition of NF- κ B by activated CREB for limiting amounts of CBP/p300, which is needed to acetylate the RelA subunit of NF- κ B, has been proposed as another pathway for attenuated production of proinflammatory mediators (139;140). Downstream in the cAMP signaling pathway, constitutive cAMP elevation by various forms of PDE inhibition efficiently impair TNF α expression and release. The isoform PDE4B was demonstrated to play a central role when macrophages from PDE4B-deficient mice were shown to elicit impaired LPS-stimulated TNF α production (141). In line with this, reactive oxygen species (ROS)-mediated TNF α response was recently reported to be more or less obliterated by PDE4 inhibitors (142).

In contrast, cAMP has been shown to potentiate the anti-inflammatory IL-10 response to LPS challenge in macrophages, boosting the release of an important factor for protection against the onset of septic shock (132;143). CREB, together with another transcription factor AP1, seems to play a role in binding to the IL-10 promoter when phosphorylated (144). Global cAMP elevation also enhances the expression of the suppressor of cytokine signaling (SOCS) 3 gene, a brake on inflammatory IL-6 production induced by IL-6 and IL-10 together, in peripheral blood mononuclear cells (PBMCs) and neutrophils (135;145).

The cAMP-mediated regulation of inflammatory mediator production in myeloid cells appears to be effected by both PKA- and EPAC1-dependent pathways. Downstream to PKA, the transcriptional regulation has been shown to involve the CRE-binding protein and CAAT/enhancer binding protein (C/EBP) transcription factors attaching to genetic promoter elements (146;147). Multiple pathways for the immunomodulatory effects of EPAC has been suggested, from its influence on extracellular matrix proteins such as laminin, fibronectin and hyaluronan that are feeding back the signal as tissue injury signals, to the involvement of ERK and C/EBP in bringing fourth the observed induction of SOCS3 (107;148).

2.4.2 Impairment of phagocytosis

Phagocytosis involves a highly regulated sequence of signal transduction events that lead to cytoskeletal and membrane rearrangement and eventually particle engulfment (90). Raising global cAMP levels in myeloid cells have been demonstrated to suppress the opsonin-dependent Complement receptor (CR) and Fragment crystallizable region receptor (FcR), as well as opsonin-

independent scavenger receptor-mediated phagocytosis (149-151). However, the mechanisms of cAMP-mediated inhibition in phagocytic function have not been completely defined. cAMP has been shown both to inhibit and promote F-actin polymerization during FcR-driven phagocytosis (152;153). Other reports point toward regulation on the level of receptor expression (149;154).

EPAC1 has also been demonstrated to mediate the cAMP-dependent reduction of FcR-phagocytosis in alveolar macrophages (155). However, reports indicate that both PKA and EPAC1 may counter-regulate phagocytosis in different cell types (151). For example, PKA seems to regulate FcR phagocytosis in circulating monocytes, while both EPAC1 and PKA inhibit this function in monocyte-derived classically activated macrophages (133).

In addition, cAMP also appears to regulate phagolysosome maturation. Increased cAMP levels decreased phagosomal formation and acidification in a PKA-dependant manner (156;157). Interestingly, several components of the cAMP signaling pathway were found to be localized to the phagosome. PDE4 was found to be colocalized with PKA in the forming phagosome in neutrophils, and both EPAC1 and Rap1, its downstream effector, associated with phagosomes containing IgG-opsonized targets in alveolar macrophages (158;159).

2.4.3 Modulation of microbicidal activity

Granulocytes contain stores of antimicrobial proteins, ROS and proteases for the purpose of tissue extravasation and bacterial killing. In order to strictly limit the release of granule content, degranulation is induced by adherence in combination with locally produced stimulators including TNF α and granulocyte-macrophage colony-stimulating factor (GM-CSF).

cAMP elevation suppresses the microbicidal capacity of leukocytes toward bacteria, viruses, fungi and eukaryotic parasites by mechanisms which are vaguely understood (133;155;160-164). In vivo, the cAMP-mediated inhibition of TNF-production will indirectly attenuate degranulation, but cAMP is also known to inhibit exocytosis of adherent neutrophils directly. In neutrophils from knock-out mice obtained by bronchoalveolar lavage, PDE4B and -4D, but not -4A, was demonstrated to regulate several aspects of their function (165).

Bactericidal ROS release is down-regulated by a myriad of cAMP-elevating agonists. This effect is associated with, and has been proposed to involve, two pivotal steps in NADPH oxidase activation, namely the phosphorylation and translocation of the cytosolic p47phox subunit (161;166;167). Both PKA and EPAC-1 activation have been implicated in the inhibition of ROS production in alveolar macrophages (155).

In the regulation of reactive nitrogen intermediate generation, cAMP levels have been found to have a pivotal, if somewhat poorly understood and possibly dual, role in regulation of iNOS expression and NO production (168-171).

2.4.4 cAMP signaling in leukocyte transendothelial migration

Leukocyte extravasation is tightly regulated by bidirectional signaling in both leukocytes and vascular epithelium. The mechanisms controlling this migration is a combination of chemokine-mediated attraction, integrin-dependent surface communication between leukocytes and endothelial cells, (rolling and adhesion), and migration across the endothelium. Regulation of the macrophage production of several leukocyte-attracting chemokines (IL-8, MIP-1 α , MIP-1 β) by cAMP plays an indirect role, but cAMP signaling in the recruited leukocytes also controls this process. cAMP signaling appears to regulate leukocyte infiltration in two opposite directions, depending on whether the downstream cAMP signaling mediator activated is PKA or EPAC (125).

Integrin-dependent cell adhesion to fibronectin have been demonstrated to be induced by cAMP via Epac-mediated activation of Rap1, and it was recently reported that loss of Epac1 in monocytes reduced activation of the α M β 2 integrin, and that Epac1 promoted monocyte adhesion to vascular endothelium (124;172). However, PKA-mediated mechanisms have been reported to inhibit extravasation of leukocytes. In neutrophils and eosinophils, induction of cAMP by the PDE4 inhibitor rolipram blocks the surface expression of α M β 2-integrin and inhibits shedding of the L-selectin CD62L, which is a prerequisite for efficient rolling (173). These effects were PKA-dependent. Integrin-dependent adhesion was inhibited by PKA, an effect lost when subcellular PKA anchoring was disrupted (174). Likewise, in monocytes, cAMP inhibits surface expression of β 2-integrins and CD62L shedding via PKA (133). As transendothelial migration requires the disassembly of the tight junctions that retain endothelial barrier function, the vital role of cAMP-signaling in maintaining vessel wall integrity should be noted (discussed more extensively later).

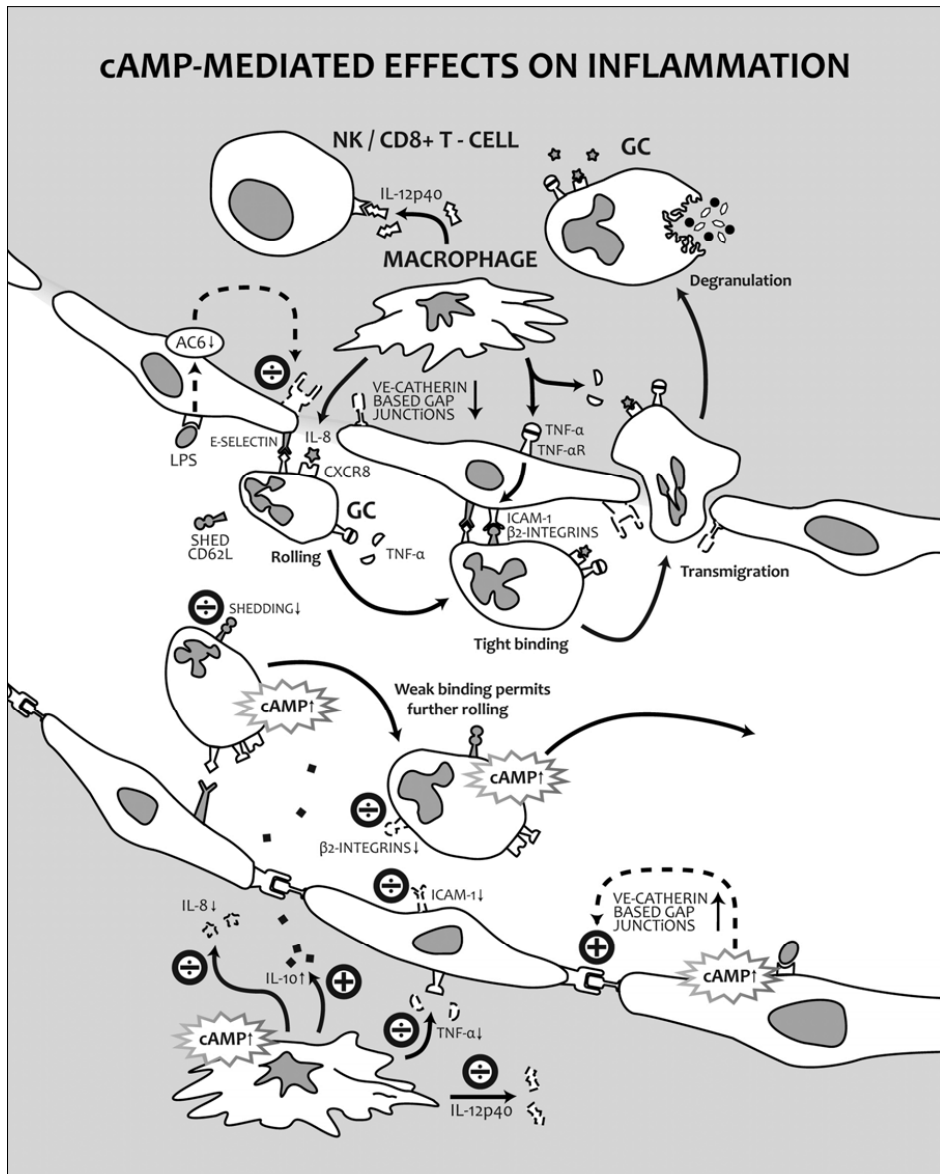


Figure 2: cAMP-mediated effects on inflammation. The cAMP signaling system plays several important roles in the innate immune response. The upper half of the depicted vessel exhibits a normal inflammatory response; endotoxin dissolves epithelial gap junctions, tissue macrophages call for circulating immune cells, and endothelial cells display adherence molecules that facilitate the extravasation of activated neutrophils that degranulate out in the tissues. The lower half depict the same situation, but with a generalized rise in cAMP levels; pro-inflammatory cytokine release is reduced, endothelial gap junctions stay intact, and fewer adherence molecules are expressed, leading less leukocyte rolling and extravasation.

2.5 Dysregulation of cAMP in sepsis and other inflammatory states

2.5.1 Altered cAMP levels in sepsis and endotoxemia

The first hints of cAMP dysregulation in sepsis came as serendipitous findings from studies of the hepatic glycogen metabolism in the 1970s, where altered cellular levels of cAMP were noted in rat endotoxemic models (175;176). Some years later, trials of prostaglandin synthesis inhibitors confirmed abnormal liver values of cAMP in dogs, as well as decreased AC responses to various GPCR ligands (177;178). Disturbances in myocardial cAMP levels during endotoxemia were also suggested to be of importance in the autonomous response to inflammation, a concept which has been revived in this decade (3;179).

In the late 1990s, comparisons between PBMCs from healthy controls, critically ill non-septic patients and septic patients revealed a 40 % attenuation of β -adrenergic receptors (β ARs) in the two latter groups, as well as reduced basal levels of cAMP. However, when cAMP production capacity was tested using the AC activating agents NaF or forskolin, there was a significantly lower responsiveness in the septic patient group attributed to a heterologous desensitization of AC activity (180). This finding was confirmed by exposing PBMCs drawn from healthy human subjects to serum from patients with severe sepsis or septic shock, which conferred reduced cAMP production potential (most markedly in the shock serum group) compared to serum from healthy controls (181).

In knock-out models of mice, the inactivation of different cell mechanisms for raising intracellular cAMP levels suggest that they may be closely linked to the development of SIRS and sepsis. Deficiency in the cAMP-inducing adenosine 2A (A_{2A}) or pituitary adenylyl cyclase activating peptide (PACAP) receptors has been shown to make mice highly susceptible to developing sepsis (182;183). PDE4B knock-outs, but not knock-outs of the highly related PDE4A or PDE4D isoforms, exhibit a marked improvement in survival after receiving a high dose intraperitoneal injection of LPS, as well as a > 50 % reduction in macrophage TNF α production (141).

2.5.2 Using cAMP pathway manipulation to evade host defences

Underscoring the importance of cAMP as a key regulator of innate immune function is the finding that several pathogenic microorganisms have evolved mechanisms to exploit host cell cAMP signaling as a virulence factor. By employing toxins that disrupt the normal regulation of cAMP production directly or indirectly, bacteria can disable host cell phagocytosis, intracellular killing and inflammatory mediator generation, all of which give them an advantageous edge in establishing infection (90;184).

Probably the best known microbial pathogen that uses cAMP amplification as a virulence factor is *Vibrio cholerae*. The cholera toxin is a heterodimer, and binding by one subunit to the cell surface results in translocation of the other subunit into the cell. When the toxin has reached the cytoplasm, it catalyzes the ADP-ribosylation of the α subunit of the stimulator G protein and facilitates constitutive activation of AC enzymes. The resulting cAMP accumulation in the gut epithelial cells is recognized as the chief cause of massive diarrhea (185). Similarly, the heat labile toxin of *Escherichia coli* exert its unwholesome effects in a resembling manner (184). Both toxins have been shown to inhibit phagocytosis, intracellular bacterial killing, pro-inflammatory mediator production and chemotaxis in myeloid cells (160;186-188).

Bordetella pertussis is a small, gram-negative bacillus that causes the highly contagious childhood disease whooping cough, and it provides an illustrative example of how overwhelming the cAMP system can derail innate immune defences (184;189). Two toxins secreted by *B. pertussis*, the PT and CyaA toxin, both act to raise host cell cAMP, albeit by separate mechanisms (189;190). The PT toxin catalyzes ADP ribosylation of the α subunit of the inhibitory G-protein, while the CyaA toxin enters the cell, is activated by eukaryotic cofactors such as calmodulin and then acts as an exogenous AC enzyme, mediating unregulated conversion of cellular ATP to cAMP. These toxins have been demonstrated to impair phagocytosis, reduce ROS generation, suppress chemotaxis and attenuate cytokine production in neutrophils and macrophages (63;191-194). Three other calmodulin-dependent bacterial AC toxins have been identified; the edema factor of *Bacillus anthracis*, the ExoY of *Pseudomonas aeruginosa* and the AC toxin of *Yersinia pestis*. In addition, *Bacillus subtilis* secretes acylpeptides that inhibit phosphodiesterases in order to raise cAMP levels (184). Taken together, these findings illustrate the diversity of cAMP manipulation techniques evolved by pathogenic microbes to incapacitate our innate first line of defense.

2.6 MicroRNA and the innate immune system

2.6.1 MicroRNAs as key regulators of cellular fate and function

MicroRNAs (miRNAs) are an abundant gene family of small, noncoding ribonucleic acids that over the last decade have radically augmented our understanding of the molecular mechanisms that regulate gene expression. Present in virtually all species, miRNA-mediated post-transcriptional repression of protein-coding genes represents a fundamental layer of genetic programming, able to exert control over diverse and complex cellular functions such as development, proliferation, differentiation, cell fate determination, apoptosis, signal transduction and the maintenance of homeostasis (195). Although not recognized as a distinct class of biological regulators until nearly a decade after first

being discovered by Ambros, Lee and Feinbaum in 1993 (196), their high conservation across eukaryotic organisms point towards ancient origins and a crucial role in genetic regulation. To date, about 700 different human miRNAs have been discovered and they are estimated to target around 60 % of mammalian genes (197). Many of the miRNAs exhibit a distinct cell- or organ-specific expression, underscoring their importance as key players in the establishment and maintenance of cell fates, and abnormalities in their expression have been observed in a wide array of human diseases (198).

2.6.2 Biogenesis and mechanism of action

Mature miRNAs are small, single-stranded RNA molecules of approximately 22 nucleotides that regulate mRNA stability and translation through antisense RNA-RNA interaction (199). In brief, miRNA genes are typically transcribed by RNA polymerase II into long primary transcripts (pri-miRNAs) that form a stem-loop structure and which can be hundreds or more than a thousand nucleotides long (195). In the most common (“canonical”) pathway, a microprocessor complex with a catalytic core composed of the Drosha and DiGeorge syndrome Critical Region 8 (DGCR8) proteins crop and polyadenylate the primary transcripts in the nucleus. Resulting from these processes are ~ 70 nucleotide precursor-miRNAs (pre-miRNAs) that are exported to the cytoplasm via a mechanism that involves exportin-5. Dicer, a cytoplasmic RNase, subsequently cleave the pre-miRNAs into ~ 22 nucleotide miRNA duplexes (200). The duplex strand with the highest base pairing stability (the ‘passenger’ strand) is then degraded, whereas the other (the ‘guide’ strand) becomes selectively loaded into a microRNA ribonucleoprotein effector (miRNP) and associates with one of the highly conserved Argonaute proteins (199;200). The best characterized miRNP is known as the RNA-induced silencing complex (RISC), and acts as a versatile mRNA-regulating platform to exert different types of regulatory responses.

The miRNA-RISC complex binds to the complementary 3'- or 5' untranslated region (UTR) of target mRNA and regulate protein synthesis by either translation inhibition (when complementary binding is partial) or deadenylation and mRNA degradation (when complementary binding is near-perfect) (195). The first mode of action implies that miRNA may alter protein expression without detectable changes in target mRNA, posing challenges to the widespread use of cDNA-based quantitative PCR. The individual miRNAs seem to have the potential to regulate multiple genes and thus, participate in larger gene networks designed to control specific biological processes (201). In addition to protein coding genes, miRNAs may target promoters, regulate the transcription factors directly, or repress genes that act as negative regulators of other genes, thus indirectly upregulating a specific target

gene (202). Through this organization, a specific miRNA is capable of effectuating widespread genetic regulation and elicit large functional changes within the cell.

However, multi-level control of the miRNA pathway complicates the efforts to clarify the functions of individual miRNAs. For example, comparison of tumor-specific mature miRNA expression with pri-miRNA transcript levels showed poor correlation and suggest that maturation is a regulated process (195). Stabilization of the cytoplasmic Dicer through MAPK/ERK-mediated phosphorylation, epigenetic mechanisms such as DNA methylation and selective usage of alternate 3'UTR isoforms by target mRNAs also represents various modifiers of the system (195;200). Our limited understanding of such miRNA-pathway regulatory mechanisms is bound to hamper attempts at *in silico* algorithmic prediction of specific miRNA effects for the time being, and does in all likelihood result in significant false positive and negative discovery rates when trying to predict miRNA-mRNA interactions by computational modeling alone. Experimental confirmation is therefore vital when a predicted miRNA-mRNA interaction is put forth.

2.6.3 The role of microRNA in immunity

Emerging evidence on miRNA is currently reshaping our understanding of intracellular immune cell regulation and coordination, revealing a level of molecular control beyond the established roles of signaling pathway mediated by kinases and transcription factors. Systematic analyses have revealed that different hematopoietic organs and cell types exhibit distinct miRNA profiles requisite for correct development, differentiation and stability of several immune cell lineages (198). Experimental evidence suggests that miRNA processes can be influenced by immune challenges, inflammation or other forms of cellular stress. In addition, miRNA have been demonstrated to regulate antigen-presentation, Toll-like receptor signaling cascades and cytokine production, immunoglobulin class-switch recombination in B cells and T cell receptor signaling, as well as proving themselves fundamental players in B and T cell development and differentiation (198;202). Signal transmission through miRNA-containing exosomes, which are specialized membranous nano-sized vesicles derived from endocytic compartments, have been proposed as a well suited mode of signal transmission when controlling space-confined processes such as the initiation of the immune reponse (203).

Dysfunctional miRNA expression has been associated with a wide variety of human diseases, including both acute and chronic inflammation as well as viral infections. A recent paper by Sonkoly and Pivarcsi (195) suggests four possible routes miRNA may contribute to or cause diseases;

- I. Loss or downregulation of miRNA expression due to mutation, epigenetic inactivation, aberrant processing or transcriptional down-regulation, allowing for uncontrolled expression of their targets
- II. Overexpression of a miRNA due to gene amplification or mutations in its promoter region or due to transcriptional upregulation, causing suppressed production of target proteins
- III. A mutation in the 3'UTR of an mRNA may affect a miRNA binding site and the miRNA may no longer be able to bind to it, resulting in overexpression of the target mRNA
- IV. A mutation in the 3'UTR of a gene may generate a new miRNA binding site, resulting in unpredictable genetic effects.

Interestingly, miRNAs encoded in the viral genome are capable of reshaping the cellular environment to maximize viral replication, hijacking the host cell miRNA machinery for its own malicious purposes. Use of miRNA has numerous advantages from a viral perspective: they can specifically down-regulate host cell genes, they occupy less than 200 nucleotides of the viral genome and they lack antigenic properties (195). For example, the presence of the liver-specific miR-122 is a prerequisite for successful hepatitis C virus (HCV) replication, and the Epstein-Barr virus (EBV) uses exosomes to transmit EBV-encoded miRNAs from infected to non-infected cells, including monocytes and T-cells (198;203).

A successful inflammatory response to infectious stimuli necessitate the induction and coordination of several hundred genes aimed at achieving pathogen clearance, while at the same time maintaining tight control of the proinflammatory cascades to prevent the process from escalating into run-away inflammation. Expression profiling of 200 miRNAs in the human monocytic THP-1 cell line revealed miR-146, miR-132 and miR-155 as endotoxin-responsive genes (204). Cell surface TLRs (TLR2, TLR4 and TLR5) all induced miR-146, while intracellular TLRs (TLR3, TLR7 and TLR9) did not elicit a similar effect. The proinflammatory cytokines tumor necrosis factor α (TNF α) and interleukin-1 β (IL-1 β) also upregulated miR-146 expression via the NF- κ B pathway. Of note, miR-146 was found to target two key adaptor proteins in the TLR/ IL-1 β pathway, namely TNFR-associated factor 6 (TRAF6) and IRAK1, suggesting that miR-146 may function as a negative feedback mechanism regulating bacterial-induced TLR-signaling (204). Further studies in THP-1 cells have revealed miR-146 to rise 4 hours after endotoxin challenge, increasing to a 35-fold upregulated expression over 24 hours (205). This could be related to monocytic lipopolysaccharide (LPS) tolerance, a phenomenon where cells that have been given an LPS-priming dose exhibits less responsiveness to new challenges for a time period. LPS-tolerant THP-1 cells were observed to regain responsiveness, as measured by TNF α production, when miR-146 decreased to normal levels after 22 hours. The same study demonstrated that

transfection with miR-146 mimicked LPS-priming, while transfection with a miR-146 inhibitor disrupted normal endotoxin tolerance (205). This mechanism also appears to be responsible for the cross-tolerance developed for non-LPS TLR-ligands after priming with LPS, and seems reproducible when using other bacterial compounds such as peptidoglycan as the priming agent (206).

In contrast to miR-146, miR-155 is strongly induced by antiviral response cytokines such as interferon- β (IFN- β) and interferon- γ (IFN- γ) (204). In T-cells, miR-155 expression has been found to be under control of the CREB transcription factor, via Fox3p, and can repress several genes in the LPS signaling pathway (FADD, IKK ϵ and Ripk1) as miR-155 targets (207;208). Fox3p induction by the cAMP signaling system has also been shown to repress expression of miR-142-3p, which targets the adenylyl cyclase 9 (AC9) isoform (209).

Another miRNA, miR-125b, have been found to be repressed by LPS-treatment both in the Raw 264.7 cell line and in primary human macrophages (207;210). This miRNA target the κ B-Ras2 3'UTR, an inhibitor of NF- κ B signaling, and thus, represses TNF α production. miR-125b have been proposed as a switch that might ensure that the LPS pathway is turned off in the absence of microbial stimuli, while an LPS-mediated downregulation allows for the initiation of the inflammatory response when needed.

Unfortunately, considerably less work focusing on the roles of miRNA in innate immune responses has been conducted *in vivo*. Using the technique of bronchoalveolar lavage on mouse lungs to harvest neutrophils after aerosolized LPS exposure, miRNA profiling demonstrated a rapid increase (peaking at 1 hour) in twelve miRNAs (miR-21, miR-25, miR-27b, miR-100, miR-140, miR-142-3p, miR-181c, miR-187, miR-194, miR-214, miR-223 and miR-224) (211). Microarray profiling of mice injected with LPS intraperitoneally found 19 miRNAs to be upregulated (among them miR-21, miR-146 and miR-155), with special attention being paid to miR-1224 targeting of Sp1 mRNA, whose coding product is a transcription factor that regulates TNF α (212). In a model of radiation-induced thymic lymphoma, TLR4 knock-out mice has substantially lower levels of miR-21 and miR-155, which coincided with a reduced inflammatory response (213).

In humans, the potential of miRNA as biomarkers for disease processes have been proposed, taking advantage of the fact that exosomal secreted miRNA is very stable in plasma. Indeed, an example of such use was illustrated recently by a study demonstrating that serum miR-146 and miR-223 may predict sepsis with both high specificity and sensitivity (214).

Over the last decade, it has become clear that miRNA are deeply involved in regulating the network of inflammatory genes that lie at the heart of sepsis. Our understanding of how this added layer of regulatory complexity interacts with the mediators of the innate immune system is still in its nascency. However, the study of miRNA is a field marked by rapid development, with increasingly precise predictions using software algorithms on their genetic structure. Thus, the discovery of miRNA offers a new avenue of therapeutic approaches, and could have the potential to substantially improve survival rates in sepsis.

3. Aims of this work

- Characterize the effects of LPS on AC isoform expression *in vivo*, *ex vivo* and *in vitro* in order to explore whether previously observed reductions of cAMP levels in sepsis are caused by reduced expression of the production enzyme.
- Investigate the ability of the cAMP signaling pathway to exert regulation of TNF α protein release.
- Examine whether the effects of LPS-injection *in vivo* can be replicated using an alternate experimental sepsis animal model, the cecal ligation and puncture procedure.
- Explore the molecular mechanisms leading from inflammatory activation (endotoxemia, sepsis) via AC isoform attenuation to reduced proinflammatory mediator production.

4. Summary of results

Paper I

We hypothesized that lower levels of cAMP during sepsis was caused by a depression in adenylyl cyclase expression, and on the grounds of available publications detailing isoform specificity in other cell populations, we wanted to examine if such was also the case in endotoxemia. We mapped the mRNA expression of AC isoforms in major organ systems in the rat, and also explored the effects mediated by 6 hours of LPS infusion on AC expression levels. In the endotoxemic rats, our observations indicated a general depression of AC mRNA expression, presumably reducing cAMP production capability. In many samples, the size of the effects was discernible. Spleen, the most richly vascularized organ we isolated, showed a near obliteration of its AC expression. AC6 was widely down-regulated in many organs, including heart and liver, but not in lung or liver macrophages. In rat liver macrophages/Kupffer cells, we demonstrated that prostaglandin E₂-mediated cAMP production was inhibited by LPS treatment, in line with a marked attenuation of AC4, AC7 and AC9 expression. Paper I was the first to report that LPS may downregulate expression of the cAMP-producing enzymes *in vivo*.

Paper II

In paper II, we sought to explore whether the attenuation of AC mRNA isoforms observed in an endotoxemic model could be reproduced in a cecal ligation and puncture model, as the latter is generally considered a closer approximation of clinical sepsis. 18 hours after the CLP procedure we found reduced expression levels of several AC isoforms in kidney, spleen and liver. The AC9 isoform, which was downregulated in all three tissues, has previously been reported to be regulated by the microRNA miR-142-3p in T-cells. We hypothesized that this regulatory mechanism may be conserved across immune cells, and when mapped the expression, we found miR-142-3p expression to be elevated in kidney, spleen, and liver, as well as in liver endothelial cells. In order to examine whether the inverse correlation between miR-142-3p and AC9 was causally related, we transfected Kupffer cells with miR-142-3p knockdown siRNA and subsequently stimulated with LPS after 24 hours. We observed that LPS treatment increased miR-142-3p and reduced AC9 expression levels in Kupffer cells *in vitro*. After transfection, the rise in miR-142-3p and corresponding drop in AC9 mRNA expression was abolished, indicating that miR 142-3p may be part of the casual pathway from LPS recognition to AC9 isoform attenuation.

Paper III

We have found a notable gender difference in LPS-mediated TNF α responses in human whole blood, showing significantly higher peak levels (6h after LPS) for young male donors (20-30 years), and sought to examine if cAMP-mediated TNF α regulation could play a role. Several cAMP-elevating agents (8-CPT-cAMP, rolipram, isoproterenol and PGE₂) all strongly inhibited the TNF α response in whole blood after LPS exposure. Based on the findings in macrophages/spleen in Paper I, we hypothesized that there may be significant AC regulation by LPS also in human monocytes. We observed that the calcium-activated AC isoforms AC4 and AC7 showed the highest expression levels in monocytes, and both were strongly attenuated after 3 hours of LPS exposure in males only. AC6 and AC9 were also expressed in human monocytes, and the same male-specific trend was observed for AC9, but not AC6. Through siRNA knock-down experiments in the human monocyte cell line THP-1, we demonstrated that AC7 and AC9 knock-down led to significantly higher LPS-mediated TNF α release, which was not observed for AC4 and AC6. The data indicate that male-specific inhibition of AC7 and AC9 may play a role in gender-differences in TNF α release.

5. Discussion

5.1 Methodological considerations

This section will discuss some of the general characteristics and pro et contra considerations of the models chosen in the present work. For a complete reference of detailed protocol, technical data or suppliers, please refer to the corresponding sections of Paper I-III.

5.1.1 Experimental animal models

In order to explore how AC isozyme expression changed in sepsis, we employed the two of the most commonly used animal models of experimental systemic inflammation, the endotoxemia model (Paper I), and the cecal ligation and puncture model (Paper II). These models are most commonly used in rodents; rats and mice. In general, the advantage of using the murine model is the possibility to study knock-out animals, whereas the size of a rat simplifies tissue analysis and cell isolation. In the endotoxemia model, the animals receive an intravenous injection of LPS over a ten minute period. Acting through the TLR4 pathway, LPS is able to reproduce most of the pathophysiological features of sepsis, causing hemodynamic collapse and multi-organ failure within 6 hours (215;216). Infusion in the central vein of a sedated animal provides for a controlled induction of the inflammatory mechanisms leading to multi organ failure and shock in a model which is widely used and validated internationally. By choosing endotoxin as our model agent, we ensure that the inflammatory response runs down-stream of the most meticulously characterized system, the TLR4 receptor. The endotoxemic model also has the advantage that the infectious stimulus is directly quantifiable and conditions are easy to standardize.

The most commonly used alternative experimental sepsis model to endotoxemia is the cecal ligation and puncture (CLP) procedure. Since its conception by Chaudry in 1979, more than one thousand scientific articles have been published using the procedure for research into septic shock (217). Using an abdominal incision, the cecum is ligated and punctured by an 18" G needle, facilitating a small droplet of feces into the abdominal cavity. Mimicking a ruptured appendix, the animals then develop peritonitis, sepsis, organ dysfunction and shock over the period of 18-24 hours. As such, the model is much closer to the clinical picture of human sepsis, which generally develops more insidiously than what can be seen in the rapid disease progression in response to LPS injection. The CLP operation produces a polymicrobial active infection, as opposed to the use of a single, non-living agent used to artificially induce shock in endotoxemia. Its noisier, but clinically more realistic picture is an advantage when testing the effectiveness of therapeutic interventions in animal trials. An added

advantage is the potential to run longer studies with hard end-points, something precluded in the sedated endotoxemic animal.

Other models exist, but are less frequently used. Urosepsis has been modeled in a model with uterine ligation and inoculation of *E. coli* (218). Some authors also use a version of the procedure where antibiotic treatment is added (219).

Neither of the models are precise representations of the human condition, which may help explain the preponderance of beneficial interventions in experimental animal research within the field, as benefits repeatedly fail to be reproduced in human clinical trials. Both models have a place in sepsis research, but results need to be interpreted with an eye for where the models resemble human clinical disease and where they do not. We believe both models have value in exploring the molecular mechanisms underlying the pathophysiological process in sepsis, and found it worthwhile to examine AC expression profiles in both models.

5.1.2 The whole blood model

The simple *ex vivo* whole blood model represents a good choice for introductory exploration of circulating immune cells and their extracellular signaling. Its simplicity and robustness allows for a wide range of experiments on the cytokine responses in a mixed white blood cell population, while the experimental set-up allows for quick expansion to a large number of research subjects if an initial pilot produces interesting observations. The model is characterized by stable leukocyte count and high viability (220). The endogenous presence of soluble factors like LBP and soluble CD14 in plasma facilitates and potentiates LPS detection by the cells of the innate immune system, with the former protein having a concentration-dependent dual role which promotes LPS-induced activation at low concentrations while it tampers LPS-stimulation when involved in the acute-phase response (221). From our vantage point (Paper III), another advantage with the model was the presence of endogenous levels of gender hormones at the time when the blood was incubated with LPS. Both the TLR4 and cAMP pathways could easily be stimulated at various steps in all the leukocytes subject to study, and their effects on inflammatory mediator release be examined (222). The whole blood model thus represented a fast and inexpensive way to study how LPS interacted with AC production capacity, and how different cAMP levels influenced TNF α release.

5.1.3 Macrophages and monocytes

Inflammation is generally initiated by the recognition of an infectious pathogen by the local immune defense system, chiefly in the form of contact with resident tissue macrophages. Although present in

every organ, the liver plays a particularly important role in the innate immune system *in vivo*, illustrated by its disproportionately abundant presence of macrophages. About 60-80 % of the total human resident macrophage population resides in the liver, where they line the narrow sinusoids and constitute 15 % of the total liver cell population (223-225). By surveying the bloodstream filtered through the organ, they are positioned to instigate the systemic inflammatory process upon recognition of infection and tissue damage. In the clinical case of a ruptured appendix, Kupffer cells will react by sending out a massive call for reinforcements by releasing cytokines and chemokines into the circulation. Chemokines allow circulating leukocytes to travel towards the originating site, and cytokines activate the cells for defusing the pathogen. Kupffer cells have been shown to be key players in initiating the shock syndrome in the CLP model (60). On this basis, we isolated primary Kupffer cells isolated after liver perfusion and cultured them for further experiments.

Monocytes and macrophages share many structural and functional similarities, as they represent different stages in the cell's development. We suspected that the regulatory cAMP pathway may be conserved across innate immune cells, and hypothesized that monocytes would be subject to similar regulation as macrophages. As monocytes are more readily available than tissue macrophages in humans, this allowed us to study human AC regulation. Combined with the simple set-up of the whole blood model, the isolation of monocytes using magnetic beads allowed us to gather samples for a substantial number of donors. Monocytes also make an interesting object of study in themselves, since the production of TNF α in LPS-stimulated *ex vivo* blood can primarily be prescribed to monocytes (226).

5.1.4 mRNA instead of protein

It is a limitation that a considerable proportion of our work consists of mRNA data without verification through protein expression. At various point during the course of our work, we have attempted to visualize the AC and cAMP pathway proteins and their interactions using fluorescence microscopy, Western blot or other protein-based methods. Unfortunately, immunodetection of adenylyl cyclase proteins is difficult both due to low levels in most cells (0.01–0.001% of membrane protein), and the lack of high quality antibodies (133;227;228). In fluorescence and confocal microscopy, the antibodies gave consistently weak signals, and we were unable to produce high-quality images due to autofluorescence from surrounding lipofuscin in the Kupffer cells, despite repeated attempts at various quenching protocols. Although we managed to identify bands on Western blots, the results were either diminishingly weak or at unexpected protein lengths, causing us to conclude that the antibodies at our disposal were not good enough for visual studies of the

behavior of the AC isozymes. For these reasons, we had to look for predicted functional results of protein regulation rather than the proteins themselves in order to complement our mRNA observations.

5.2 Adenylyl cyclase regulation in monocytes/macrophages and the inflammatory response

5.2.1 Attenuated AC expression in monocytes and macrophages: Role in sepsis/endotoxemia?

As elaborated upon in the introductory section, there is an ample literature underscoring how intracellular cAMP signaling is a sinewy regulator of inflammatory responses in monocytes and macrophages. In the present work, we explored LPS-mediated regulatory effects on AC expression in rat Kupffer cells and alveolar macrophages, as well as in human *ex vivo* monocytes.

In paper I we reported that rat Kupffer cells isolated after 6 hours of endotoxemia were inhibited with regards to AC expression, with the isoforms AC4, AC7 and AC9 all being significantly attenuated compared to cells from sham-operated animals. In paper II we found similar AC attenuation in Kupffer cells 18 hours after being subjected to a polymicrobial model, with reductions in AC4, AC5, AC6 and AC9. Rat alveolar macrophages, on the other hand, had less pronounced alterations in response to LPS and AC5 was the only isoform where downregulation was statistically significant. The pathological process of endotoxemia is one defined by massive release of proinflammatory mediators, followed by rapid progression of systemic inflammation and organ injury in the course of a mere 6 hours (229). In contrast, the course of sepsis induced by the CLP procedure is markedly slower, with organ injury markers rising later and more gradually (230).

From our data it is not possible to draw definite conclusions as to whether the observed differences between the results are due to the characteristics of the model, differences in the cell populations or temporal aspects of the sampling. However, both experiments indicate that the reduced levels of cAMP in peripheral blood monocytes, shown to be a feature of both septic patients and healthy donors exposed to septic serum, may be caused by impaired production of cAMP by adenylyl cyclases (180;181). To explore this possibility (Paper III/Manuscript I), we exposed human full blood to LPS *ex vivo* for 3 hours before isolating monocytes. In male donors, we observed significant reductions in monocyte AC4 and AC7, as well as a trend ($p = .048$) towards attenuation of AC9. No such statistically significant association was evident in females, and a few (2-3 out of 17 for each AC isoform) even exhibited a 4-8 fold increase.

As discussed in the introductory section, an important attribute of the cAMP second messenger system is its capability of delivering a precise, spatially confined signal through subcellular compartmentalization (95). The individual roles of the AC isoforms are poorly characterized in immune cells, but their different regulatory properties may provide clues. For example, PGE2 and forskolin differ in their capacity to activate AC9, which the latter fail to induce (134). We found that pretreatment with LPS had discriminatory effects on the stimulatory power of these agonists, a finding which has also been shown by others (231). This finding suggests a role for AC9 in PGE2-mediated signaling. In a trial of administering marrow to sepsis patients, PGE2 was recently ascribed a key role in stimulating monocyte and macrophage IL-10 production (232). Immunofluorescent techniques have identified a pathway from PGE2 through EPAC1 which colocalized with micro-tubuli organizing centers (MTOCs) and mediated FcR-phagocytosis (159;233). Macrophage levels of cAMP has been closely implicated as core regulators of their internal physiology, and manipulation of cAMP can transform classically activated (M1) macrophages to resolution-phase macrophages (rM) when levels are heightened, et vice versa (234).

From previous work in our lab, we know that AC9 is highly expressed in Kupffer cells, and that cAMP signaling can attenuate TNF α release (134). It was also recently demonstrated that mice deficient in AC7 have macrophages that generate a weaker cAMP response to inflammatory stimuli and respond to LPS challenges with increased TNF α release, causing them to become hypersensitive to endotoxemic shock (235). In THP-1 cells, knock-down siRNA directed against AC7 and AC9 expression effectively doubled the TNF α release in response to LPS, while transfection with AC4 and AC6 did not (236). There were also indications that the PDE4-selective inhibitor rolipram had diminished anti-inflammatory effect (Supplemental figure), which would be consistent with impaired production capacity in the subcellular isoform-specific cAMP pools.

In summary, we find that our experiments corroborate earlier observations by our own group and others underscoring the importance of the AC7 and AC9 isoforms as contributors to inflammatory mediator release. As far as we know, we are the first to demonstrate the effects of both AC7 and AC9 on TNF- α release in a human monocytic cell line

5.2.2 miR-142-3p and AC9 downregulation

The decrease in AC9 expression observed in the CLP model (Paper II), led us to explore the expression level of miR-142-3p in organs and the main liver cell populations in the aftermath of CLP (237). At 18 hours, we found significant increases in the liver, kidney and spleen that correlated with reduced expression of AC9 mRNA. This was also true when we examined miR-142-3p and AC9 in Kupffer cells

and LSEC cultures. Based on these findings, we hypothesized that AC9 mRNA and protein expression was downregulated by miR142-3p in innate immune cells, analogous to the regulatory pathway observed in T-cells. When we transfected primary rat Kupffer cells with miR-142-3p antagomir, we found this manipulation to effectively prevent the LPS-mediated AC9 attenuation otherwise witnessed in control cells transfected with scrambled siRNA (238;239).

MicroRNA, virtually unknown merely a decade ago, swiftly evolved from scientific curiosity to the point where it is shifting our paradigms of genetic regulation. They have proved themselves to be crucial players in a wide range of cellular functions, and the experimental evidence indicate that they exercise key functions in facilitating normal immune responses as well. Although the emergence of microRNA-mediated regulation will not make the understanding of intracellular signaling networks any easier, they do provide new avenues of approach for diagnosis and therapy. Given our current knowledge, it seems a safe prediction that the use of microRNA for clinical applications will rise quickly in the coming years, and that targeting of disease-related microRNA has the potential to give rise to radically new treatment principles for a wide array of pathological conditions.

As microRNA is considered to be an evolutionary ancient component of genetic regulation with high conservation rates, we hypothesized that some functions might also be conserved across different populations of immune cells (197). AC9 had recently been shown to be highly expressed in regulatory T-cells, and appear linked to their suppressive function (240). The same study demonstrated that miR-142-3p target the 3'-UTR (untranslated region) of AC9, and thus lead to reduced expression levels of isozyme mRNA and protein. All hematopoietic cell lineages have been found to have abundant expression of miR-142-3p, where the microRNA appears to be preferentially expressed (241).

Several microRNAs have been implicated in inflammatory diseases, and elevated levels of plasma microRNA have previously been associated with liver injury and sepsis (214;242-244). In diseases where cAMP activity has previously been shown to be dysregulated, such as psoriatic skin and multiple sclerosis patients, other investigators have found expression of miR-142-3p to be elevated in inflammatory phases, implicating it as a potential pathological agent or intermediary that could lead to loss of appropriate AC9 function (242;244).

Since our experiments, others have found miR-142-3p to have important roles in myeloid differentiation, directly inhibiting cyclin T2 and TGF- β activating kinase binding protein 2 genes, and decreased cAMP levels with weakened PKA activity in response to increased miR-142-3p has been reproduced in primary cells from acute lymphoblastic leukemia patients (245;246). Meanwhile, it has

also been reported that IL-10 knock-out mice have higher baseline miR-142-3p expression in circulating leukocytes, with increasing miR-142-3p levels corresponding with worsening inflammatory pathology resulting from the lack of IL-10 (247). Exogenous IL-10 exposure failed to restore miR-142-3p levels to normal levels. A study published earlier this year found that peripheral blood mononuclear cell content of miR-142-3p correlated with operational tolerance, and proposed the existence of a negative feedback loop involving miR-142-3p to maintain this tolerance (248). The same study overexpressed miR-142-3p in the Raji B-cell line, where it was discovered to regulate almost a thousand mRNA transcripts, of which 49 have known roles in inflammation.

At the same time as we conducted our experiments, another group examined the effect of miR-142-3p on IL-6 in mouse dendritic cells and reported the somewhat conflicting finding that IL-6 seemed to rise with miR-142-3p knock-down (249). However, when performing *in vivo* transfection with miR-142-3p, TNF- α mRNA and protein expression were both significantly reduced in wild-type mice subjected to antagomir, and silencing miR-142-3p also improved overall survival in response to endotoxemia.

Taken together with the previously discussed differential role of the AC9 isozyme in the regulation of proinflammatory TNF α and anti-inflammatory IL-10, we conclude that an increase in miR-142-3p after CLP appears to lead to a reduction of AC9 and weakening of spatially relevant cAMP production in macrophages, tilting the innate immune system in a direction of aggregated and inappropriate proinflammatory response (234). In the context of the initial proinflammatory phase of severe systemic inflammation, we therefore propose that high levels of miR-142-3p in innate immune cells may be associated with more severe outcomes. The cAMP pathway regulates anti-inflammatory polarization of macrophages to healing and reparation during the secondary response, and miR-142-3p may have a role in reversing this.

5.3 Potential implications of AC regulation in different tissues

5.3.1 Attenuation of AC expression after LPS-exposure

In paper I, one of the main findings was a marked reduction in the mRNA levels of most adenylyl cyclase isoforms after 6 hours of endotoxin infusion in the rat, with some indication of differential regulation in various organs and cell populations. Within this time frame, the animals developed multiple organ damage, as assessed both morphologically and by markers of liver and kidney injury (60). For paper II, we hypothesized that AC expression would also be attenuated in a model of bacterial infection and sepsis. The CLP model is intended to mimic the clinical situation of a septic

peritonitis, with markedly slower progression than the clinical course caused by infusion of LPS. Still, systemic inflammation and organ injury (as determined by plasma values of commonly used biochemical markers) was decidedly evident at both 10 and 18 hours (237). We found that the changes in AC mRNA expression from CLP sepsis did resemble those observed in endotoxemia, giving the impression of a broad and widespread downregulation of the cAMP producing isozymes.

As we have already pointed out, there are numerous studies demonstrating that global cellular levels of cAMP are reduced in response to endotoxemia and sepsis both among animals and humans (175-178;180;181). The widespread attenuation of AC isozyme expression after LPS injection or exposure to a polymicrobial infection observed by us would provide a plausible cause for the decreased cAMP levels described by others. Unfortunately, knowledge of the specific roles of individual ACs is scarce in many tissues or cell populations; however, substantial advances have been done within heart and endothelial barrier research with regards to our understanding of this system. In this section, we will review and discuss the literature with regards to the potential implications of the observed reduced cAMP production capacity in select tissues.

5.3.2 AC isoform regulation in the heart

In paper I, we found the mRNA levels of AC6 to be significantly down-regulated in heart tissue from endotoxemic animals, with mean expression levels close to a quarter of the sham operated group (215).

The cAMP system has an important role in the heart; not only does it regulate the heart rate by mediating external catecholaminergic signals, but it also regulates the functional response to a plethora of other hormones and neurotransmitters (96). Cardiac myocytes primarily express two isoforms of ACs, AC5 and AC6 (250). While AC6 is expressed in most tissues at a low level, AC5 appears to be most abundant in only two; brain and heart (251;252). There are indications that the isozymes are developmentally regulated in an opposite manner, with AC6 declining gradually with age from high fetal levels and AC5 following a complementary pattern (253;254). Through a series of knock-out investigations, their roles are gradually being elucidated and disruption of spatial control of the signal seems crucial in the development of heart pathology (96;255;256).

Experiments indicating that failing myocardium have reduced amounts of basal cAMP and an impaired AC functionality in response to agonist stimulation (257;258). AC5 appear to be crucial for normal heart functions, with experimental induced deficiencies producing deleterious effects, while a reduction of AC6 mRNA in the failing ventricle precipitate a drop in left ventricle (LV) contractile

function (251;254;255;259). Cardiac-directed expression of AC6 in transgenic mice shows no increases in baseline heart rate and contractile function or detectable abnormalities at advanced age, despite a 20-fold excess of protein. However, hearts exhibited a marked increase in heart rate and contractile function in response to β AR stimulation, in line with previous *in vitro* reports from the same group indicating AC (and not β AR) as the rate-limiting step in cAMP generation (260;261). *In vivo* studies of mouse models of acute myocardial infarction and cardiomyopathy associated AC6 expression with increased LV contractile function, reduced mortality and reduced incidence of high-grade atrioventricular (AV) node block (262-265). Indeed, AC6 has been shown to be expressed in the AV node and facilitate nodal anterograde and retrograde conduction without altering sinus node conduction (266). Last year, it was reported that a tet-regulated AC6 overexpression model activation exerted beneficial effects even when the gene was turned on five weeks after the establishment of severe chronic heart failure (CHF), subsequently improving function of the failing heart (267).

There has been some speculation in the cardioprotective mechanisms of AC6 overexpression (227). In cardiac fibroblasts, AC6 was recently demonstrated to be completely compartmentalized in lipid raft domains where it was activated solely by coresident GPCRs (268). A similar situation may be present in cardiac myocytes. Expression of AC6 through adenovirus-mediated gene transfer to cultured myocytes and through an *in vivo* cardiomyopathic setting has suggested a decrease in phospholamban (PLB) expression, possibly by marked upregulation of activating transcription factor 3 (ATF3) (269). ATF3, a transcriptional suppressor, binds to and inhibits the PLB promoter (270). However, AC6 expression was also associated with increased phosphorylation of both PLB and Akt (227;269). Recently, a report describing AC6 knock-out mice showed that although basal cAMP levels were normal, there was a markedly decreased responsiveness to cAMP-elevating agents such as isoproterenol, forskolin and the forskolin-derivative colforsin, and AC6 deletion also impaired Ca^{2+} -mediated inhibition of AC activity. The disruption of normal AC6 expression also proved to have profoundly negative effects on LV calcium handling, with significant reductions in PLB phosphorylation and SERCA2a activity, and conspicuous abnormalities in calcium transient formation by caffeine stimulation was interpreted as evidence for marked impairment of SR calcium storage capacity (271).

As these changes are predicted to increase intracellular calcium availability and LV contractile function, the LPS-mediated attenuation observed in heart AC6 mRNA levels after 6 hours of infusion could be presumed to be correspondingly detrimental to heart function in shock (269). In addition, there is a close scientific linkage between β AR (and hence, sympathetic) responsiveness and level of

AC6 mRNA in cardiomyocytes, which could be hypothesized to underlie the clinical observation of desensitization to vasoconstricting drugs during intensive care treatment for septic shock (3;227).

5.3.3 AC and cAMP in the maintenance of endothelial integrity

In our initial paper (Paper I) we observed widespread LPS-mediated down-regulation of AC6 mRNA expression in several richly vasculated organs (215). These findings spurred more specific examination of this isozyme in Paper II, where we examined cultures of isolated liver sinusoidal endothelial cells (LSEC) levels 18 hours after LPS stimulation and found AC6 to be approximately 26% of the level in control cultures (237).

The endothelial cell (EC) layer forms a semi-permeable dynamic barrier between the vascular space of blood vessels and underlying tissues. Under normal conditions, ECs tightly adhere to each other and interact only fecklessly with the cells circulating in blood. Upon exposure to inflammatory mediators, a disassembly of adherence junctions occur, the endothelial cells reversibly rounds up, and the expression of surface receptors that interact with circulating leukocytes is induced (272).

This change in the endothelium allows transendothelial migration of leukocytes, and is also responsible for the extravascular leakage in septic shock. In addition to its previously discussed ability to attenuate the expression of adhesion molecules, a heightened cAMP level is demonstrated to play an important role in maintaining the endothelial barrier. The inflammatory changes in endothelial structure and function are oppositely regulated by two intracellular signaling mediators, calcium and cAMP. Intracellular calcium promotes the disassembly of adherence junctions and extravascular leakage, whereas cAMP signaling preserves the junctions (273).

Notably, the adherence junctions in the endothelium are shown to be contained by cAMP-dependent mechanisms in an AC6-specific manner, mediated by both PKA and Epacs (122;274;275). PKA appears to have the most central function in inhibiting several of the calcium-mediated effects, including the stress fiber formation leading to morphological changes, and the translocation of focal adhesion proteins involved in gap formation (273). The AC6 isoform is sensitive to calcium-mediated inhibition, which may explain why intracellular calcium disturbs cAMP-mediated protection of the endothelial barrier (276). The protease thrombin, which is activated in septic shock and induces blood coagulation, is a particularly potent inducer of interendothelial gap formation (272). The endothelial protease-activated receptor of thrombin (PAR1) not only induces calcium, but also directly inhibits AC activity by releasing inhibitory G-protein (277).

It is important to note that liver sinus endothelium differs from vascular endothelium. LSEC form a fenestrated monolayer at the inside of the sinusoids, acting as a barrier between the blood flow and the perisinusoidal space (278). The open pores of the LSEC fenestrae makes permeability high compared to other microvascular endothelial cells, and facilitate the flow of soluble macromolecules from the circulation for hepatic clearance. Unfortunately, primary LSEC are not amenable to long-term culture and lose their phenotype within days after being extracted (279). The junctional complexes between adjacent LSEC cells are of a distinct molecular composition, consisting of a mix of junctional proteins shared with other endothelial populations and novel proteins reserved for LSEC alone (278-280). However, the first comprehensive analysis of its molecular structure published earlier this year concluded that human LSEC assemble the same molecular complexes typical of endothelial adherens junctions, and abundantly express the main transmembrane component, VE-cadherin, on both mRNA and protein levels at similar locations as other endothelial cells, disproving the notion that LSEC lack interendothelial junctions (278). LSEC also express all members of the family of junctional adhesion molecules, but human cells lack expression of the occludin protein commonly found in tight junctions (278).

Both Paper I and II suggest that LPS has the potential to cause widespread AC6 attenuation across multiple organs, including the observed reduction of AC6 expression levels of liver endothelium. If additional subpopulations of endothelial cells could be confirmed to respond in the same way to LPS, this would suggest that the loss of endothelial integrity, increased permeability, extravascular leakage and ultimately, hypotensive shock, may be due to AC6 down-regulation induced by LPS.

5.3.4 Reduced AC expression in spleen

The most conspicuous reductions in mRNA expression for all AC isozymes except AC5 were observed in spleen after LPS infusion (215). With the CLP procedure, a marked drop could be measured in the two isoforms most closely associated with immunological effects, AC7 and AC9 (237).

Unfortunately, earlier inquiry aimed at understanding the cAMP signaling system in spleen has been extremely sparse. However, possible implications may be speculated upon on the basis of the physiological role of the spleen itself. The spleen is an immunological and hematological organ, and contributes significantly to the production of pro- and anti-inflammatory cytokines (281). For example, splenectomy results in dramatic attenuation of the normal IL-6 response, making individuals susceptible to blood-borne bacterial infections, and in vitro measurements of lymphocyte signaling responses indicate that the normal CREB, EKR1/2 and p38 downstream response is absent (281). The spleen is also a reservoir of various immune cells responsible for innate and adaptive

immunity, boosting their numbers in circulation during the infectious response. That splenectomized individuals are at a higher risk for myocardial heart disease decades later, underscores the important role of the spleen in normal immunological homeostasis (282).

The denotative obliteration of all identifiable ACs besides AC5 strongly suggest a response in immune cells, as the tissue harvesting was performed without perfusion and these constitute a major component of the baseline spleen composition. As the cells of the immune system share a wide spectrum of common evolutionary features, part of the response may also be due to regulation of the large population of B- and T-lymphocytes. In both the endotoxemia and CLP experimental models, AC9 expression levels were markedly reduced compared to sham. AC9 has been reported to be specifically involved in polarization of T-cells towards regulatory T cells (283), which would also imply the suppression of T-cell proinflammatory cytokine inhibition. Together with AC7, attenuated levels of both isozymes may suggest that normal anti-inflammatory macrophage polarization is being inhibited.

cAMP signaling not only modulates inflammatory cytokine release from macrophages, but also serves as an inhibitory factor in a wide range of inflammatory responses, including the inhibition of leukocyte-endothelial interactions, neutrophil transmigration and degranulation, cytotoxic responses of NK-cells and T-cells, platelet aggregation and the maintenance of gap junctions. Thus, the dramatic fall in rat spleen AC expression 6 hours after LPS infusion indicated that blood cells had lost substantial cAMP production capability, and that the systemic pro-inflammatory process had spiraled out of control.

5.3.5 Reduced AC expression in liver

The narrow sinusoids of the liver are important areas of host defense against systemic infection, as the dominant population of stationary tissue macrophages reside in the liver as Kupffer cells (284). The sinusoidal endothelium is characterized by being particularly “sticky” to leukocytes and independent of a functional leukocyte rolling step for adhesion, in addition to being discontinuous with fewer tight junctions compared to vessel endothelium elsewhere (285). These features, together with the fact that activated KC and LSEC are very efficient producers of leukocyte-attracting chemokines, make the sinusoids particularly prone to leukocyte accumulation (286). Liver also contain a large population of resident NK-cells (287).

Although hepatocytes express a number of PRRs, they did not appear to be important targets for AC mRNA regulation in the sepsis model, as no significant differences in AC expression were found in

pure hepatocytes isolated from CLP and sham animals. No significant changes were found in the LSEC cultures, although there was a tendency towards a shift in AC expression from calcium-inhibited isoforms (AC5, AC6, AC9) in cells from sham animals to calcium-insensitive isoforms (AC4, AC7) in cells from CLP, which is interesting, since calcium and cAMP signals together control endothelial permeability under inflammatory conditions, as discussed in 5.3.3 (288). As already mentioned, AC6 has been demonstrated to have a critical role in the maintenance of endothelial gap junctions, and the Epac-regulated adhesion protein VE-cadherin is abundantly expressed in the interendothelial junctions (278;289). It is therefore reasonable to speculate that a shift away from AC6 expression may increase the trans-sinusoidal barrier permeability, contributing to the clinical state observed during the systemic inflammatory response syndrome.

5.4 Adenylyl cyclases as a source of gender differences in the inflammatory response

As we explored TNF α release in the ex vivo human whole blood model with regards to cAMP signaling, it became clear that males had a substantially stronger TNF α response than females at both 3 and 6 hours (236). This induced us to examine the AC isoform expression profiles stratified by gender. At 3 hours, AC4, AC7 and AC9 had all undergone considerable down-regulation, compared to no or minimal change in females. No gender-specific TNF α response was observed when examining older (post-menopausal) individuals.

Our observations are in line with a comparatively large study of 154 healthy volunteers aged around 20 to 30 years found males to produce significantly more TNF α , IL-1 β , IL-6 and IL-8 in response to a set challenge of 1 μ g/ml LPS (290). However, others have found no difference (although the endotoxin dose given was 2 ng/ml) or even a stronger pro-inflammatory response among females in a small (30 individuals of 22 \pm 1 years) study (83;84). The potential cyclic component of the female immune response indicates that results should be stratified by contraceptive use and stage of the menstrual cycle, although this was inadequately done in two of the studies (83;290;290;291).

A study of fifty subjects of 65 years of age or older with concurrent young (21 to 40 years) controls reported smaller, but statistically insignificant, release of TNF α at 6 hours in young females compared to males, and a substantial rise in TNF α and IL-6 levels in old, post-menopausal women compared to the younger group (292). Both observations are in line with the findings from the present work.

The difference between pre- and postmenopausal women suggests female hormones as a potential cause for the gender differences in AC expression. Estrogen replacement given to postmenopausal

women before intravenous endotoxin challenge attenuated the pro-inflammatory rise in TNF α and IL-6 levels, and published data from younger donors suggest that human circulating IL-6 response is decreased by estrogen (293-297). In contrast to the conflicting reports from human studies, results obtained from experimental animal studies clearly point to a female, estrogen-mediated advantage in sepsis (77;298). We conducted a computer based search on the promoter sequences of the human AC4 gene (Chromosome 14q12) and the AC7 gene (Chromosome 16q12-13), which exhibited the most evident male-specific inhibition. The promoters of both genes were found to contain putative binding sites for estrogen receptor (ER) α , and for the estrogen-induced transcriptional repressor δ EF1/ZEB (299;300).

While a homozygote knockout for AC7 is not compatible with life, heterozygote AC7 +/- mice are reported to express reduced levels of AC7 mRNA, with their macrophages producing increased levels of TNF α (301). In line with this, they are also hypersensitive to endotoxemic shock (235). Our experiment with repression of AC7 and AC9 isoforms using siRNA and nucleofector transfections in THP-1 macrophages led to a stronger TNF α release 6 hours after stimulation with LPS. That AC9 expression appears linked to TNF α regulation in monocytes or macrophages has to our knowledge not previously been demonstrated, but the possibility was suggested in a previous study in rat Kupffer cells (302). Taken together, these studies imply that gender-specific regulation of AC expression levels would produce gender differences in the TNF α response, which matches what is seen in our data.

As should be evident by now, the second messenger system modulates more than cytokine release from macrophages; cAMP signaling inhibits leukocyte-endothelial interactions, neutrophil transmigration and degranulation, cytotoxic responses of NK-cells and T-cells, platelet aggregation, and stabilizes intercellular gap junctions (108;303-308). This wide spectrum of downstream functional consequences reminds us that LPS-mediated AC regulation may yet further unexplored mechanisms of action. Further studies will hopefully reveal if and the gender-specific regulation of AC mRNA expression by LPS involves estrogen-regulated mechanisms or other gender hormone-mediated effects at the AC promoters.

5.5 Potential implications for future treatment of sepsis

It has become increasingly clear that the cAMP pathway is intrinsically involved in balancing the immune response, and interest in novel ways of manipulating the subcellular pools has been steadily rising. Two fairly recent reviews discuss the untapped potential of drug discovery by supply-side

regulation through development of isoform-specific AC agonists and inhibitors (309;310). To the list of suggested uses for such compounds – which currently include analgesics without dependence, memory enhancement, male contraceptives, and drugs for asthma and congestive heart failure – we propose to add sepsis. Although efforts are ongoing in identifying selective compounds for regulating the individual AC isoforms, their development is hampered by the high degree of evolutionary conservation between the isozymes (309-311).

The most successful anti-inflammatory cAMP-directed drugs to date are various inhibitors of the PDE isozymes. For a long time, naturally occurring PDE inhibitors like the methylxanthines theophylline and caffeine have been known to express immunomodulating properties (312). Pentoxifylline, or PTX [1-(5-oxohexyl)-3,7-dimethylxanthine], is a methylxanthine derivate and PDE4-specific phosphodiesterase inhibitor that has been shown to decrease transcription of TNF α in endotoxemia, attenuate release of pro-inflammatory cytokines such as IL-1 β , -6 and -8, lower the pool of circulating neutrophils, inhibit granulocyte adherence and transendothelial migration, reduce neutrophil degranulation and release of matrix metalloproteinases and ROS; thus, shifting the whole process towards anti-inflammation and restoration (313-318). Thus, it should be no surprise that PTX has been demonstrated to blunt endotoxin-mediated lung injury, liver damage and acute renal failure, and increase early survival in animal models of septic shock (319;320).

However, uncertainty about the right therapeutic windows (with regards to both timing and dosage) and side effects limits its clinical use. The development of inhibitors with subtype specificity could reduce the problems associated with unselective phosphodiesterase inhibition (321). Macrophages from PDE4B deficient mice indicate that many of the immunomodulatory functions of cAMP appear to be closely linked to this isoform, while knocking out PDE4A or PDE4D showed no such effects (141). A highly selective PDE4B inhibitor has been patented and was being developed for use in lymphoma under the name PLX513, but is currently listed as discontinued by the patent-holder (322). The compound would be an interesting candidate for new treatments not only for sepsis, but also from a range of diseases where unselective PDE4-directed drugs have already demonstrated efficacy; asthma, COPD, psoriasis, rheumatoid arthritis, inflammatory bowel disease, lupus and multiple sclerosis (323-325).

Another promising approach is the possible future use of miRNA-based interventions to achieve targeted immunomodulation in sepsis. An important characteristic of miRNA is that they often control a functionally related cluster of genes, and thus they may serve as switches for larger gene networks aimed at controlling specific biological processes (201;326). In 2008, the first phase I study

of hepatitis C treatment using an antagomiR against the oncogenic mir-122, which also facilitates viral replication, was initiated, and after the trial's successful conclusion, phase II was announced in 2010 (327). So far, the most common strategy has been to focus on specific miRNA shown to be strongly linked to a single pathogenic process (328). These can be knocked down using either antagomiRs (RNAs conjugated to cholesterol bound to phosphorothiotate), "locked nucleic acid" (LNA) constructs, and "miRNA sponges" (competitive inhibitors with multiple binding sites for miRNAs) (329-331).

However, impediments remain before miRNA-based therapies are ready for use in clinical practice. Delivery to the cell has been problematic *in vivo*, as artificial miRNA probes tend to activate endogenous TLR-receptors, triggering the inflammatory response (326). Also, the nucleic acids are negatively charged and do not easily cross the cell membrane, leading to proposals of encapsulation of the oligonucleotides in liposomes and the use of viral vectors (332). As recently as July 2012, Nature published a study demonstrating how viral delivery of miR-196s was able to ameliorate a serious neurodegenerative and neuromuscular disease in experimental animal models (333).

Our experiments, and the work of others, indicate that targeting miR-142-3p may improve survival in sepsis; blocking the rise in miR-142-3p should blunt the reduction in AC9 mRNA expression, and thus, mitigate the TNF α release from innate immune cells, lessening the chance of the inflammatory process spiraling out of control (237;249). As miRNA probe delivery technology improves, small nucleotide interventions that suppress the miR-142-3p rise in sepsis would be interesting candidates for treatment trials.

In conclusion, the cyclic AMP signaling system is emerging as an important regulator of the innate immune response. Its subcellular structure in cells of the immune system is still poorly understood, and the specific roles of each individual component need to be established. However, a deepened understanding of this complex, but seemingly protective, intracellular signaling system may bring fruitful therapeutic interventions not only to patients suffering from sepsis, but also bring benefits to a wide range of inflammatory diseases.

6. References

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7. Paper I

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8. Paper II

Risøe PK, Ryg U, Wang YY, Rutkovskiy A, Smedsrød B, Valen G, Dahle MK. *Cecal ligation and puncture sepsis is associated with attenuated expression of adenylyl cyclase 9 and increased miR142-3p*. Shock 2011 Oct;36(4):390-5.

9. Paper III

Risøe PK, Rutkovskiy A, Ågren J, Kolseth IB, Flood Kjeldsen S, Valen G, Vaage J, Dahle MK. *Gender differences in TNF α responses are associated with attenuated adenylyl cyclase expression in male monocytes*. Manuscript submitted for publication.